EXHIBIT B

Claim Amendment: Pending Claims After Entry of Instant Amendment

21. (Twice amended) A method for identifying the presence of cancerous cells in a human sample wherein said method comprises:

(a) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample and in a control sample of non cancerous cells by:

(1) contacting RNA from said sample and said control sample with a pair of primers, wherein said pair of primers consists of a first primer which hybridizes within exon 8 of the hTERT gene and a second primer which hybridizes within, upstream or downstream of exon 8 of the hTERT gene;

(2) amplifying the nucleic acid sequence;

(3) measuring the generation of amplification products;

(4) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample from the results obtained in step (3); and

(b) identifying the presence of cancerous cells in said sample if the quantity of hTERT mRNA comprising β-region coding sequence in said sample is greater than the quantity of hTERT mRNA comprising β-region coding sequence in said control sample.

28. (Amended) The method of Claim 21, wherein said second primer hybridizes upstream of exon 7 of the hTERT gene.

29. (Amended) The method of Claim 28, wherein said second primer hybridizes within exon 6 of the hTERT gene.

30. The method of Claim 21, wherein said second primer is SYC1118 (SEQ ID NO:5), SYC1076 (SEQ ID NO:2) or SYC1078 (SEQ ID NO:3).

31. (Amended) The method of Claim 21, wherein the second primer hybridizes within exon 8.

32. (Amended) The method of Claim 21, wherein said first primer is SYC1097 (SEQ ID NO:4).

33. (Amended) The method of Claim 21, wherein the second primer hybridizes within exon 9.

35. The method of Claim 21, wherein the amplification reaction is a polymerase chain reaction.

36. The method of Claim 21, wherein step (3) is carried out using a probe that is complementary or substantially complementary to said amplification products.

37. The method of Claim 36, wherein said probe is selected from the group consisting of CS12 (SEQ ID NO:6), CS1 (SEQ ID NO:7) and CS3 (SEQ ID NO:8).

38. (Twice amended) A kit for identifying cancerous cells in a human sample, comprising a pair of primers, wherein said pair of primers consists of a first primer which hybridizes within exon 8 of the hTERT gene and a second primer which hybridizes within, upstream or downstream of exon 8 of the hTERT gene and instructions for identifying cancerous cells.

39. (Amended) The kit of Claim 38, wherein said second primer hybridizes upstream of exon 7 of the hTERT gene.

40. (Amended) The kit of Claim 39, wherein said second primer hybridizes within exon 6 of the hTERT gene.

41. (Amended) The kit of Claim 38, wherein said second primer is SYC1118 (SEQ ID NO:5), SYC1076 (SEQ ID NO:2) or SYC1078 (SEQ ID NO:3).

42. (Amended) The kit of Claim 38, wherein said first primer is SYC1097 (SEQ ID NO:4).

43. (Amended) The kit of Claim 38, further comprising a probe which hybridizes at a sequence encompassing the exon 7-exon 8 splice junction.

44. The kit of Claim 38, further comprising a probe selected from the group consisting of CS12 (SEQ ID NO:6), CS1 (SEQ ID NO:7), or CS3 (SEQ ID NO:8) and instructions for identifying cancerous cells.

45. The kit of Claim 38, comprising a pair of primers SYC1118 (SEQ ID NO:5) and SYC1097 (SEQ ID NO:4), a probe that is CS12 (SEQ ID NO:6) and instructions for identifying cancerous cells.

46. (New) The method of Claim 21, wherein step (2) additionally comprises amplifying the nucleic acid sequence in the presence of a probe which hybridizes to the nucleic acid sequence.

47. (New) The method of Claim 46, wherein the probe is labeled.

48. (New) The kit of Claim 38, further comprising a probe which hybridizes to a sequence which is amplified by the first and second primers.

49. (New) The kit of Claim 38, wherein the probe is labeled.